

TECH CENTER 1600/2900

1636
SEP 13 2001
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/145,916B

DATE: 08/02/2001

TIME: 17:02:05

Input Set : A:\145916.txt

Output Set: N:\CRF3\08022001\I145916B.raw

#17

SEQUENCE LISTING

1 (1) GENERAL INFORMATION:

2 (i) APPLICANT: Simons, Michael

3 Volk, Rudiger

4 Horowitz, Arie

5 (ii) TITLE OF INVENTION: Stimulation of angiogenesis

6 via enhanced endothelial expression of syndecan-4

7 core proteins

8 (iii) NUMBER OF SEQUENCES: 23

9 (iv) CORRESPONDENCE ADDRESS:

10 (A) ADDRESSEE: David Prashker, Esq.

11 (B) STREET: P.O. Box 5387

12 (C) CITY: Magnolia

13 (D) STATE: Massachusetts

14 (E) COUNTRY: USA

15 (F) ZIP: 01930

16 (v) COMPUTER READABLE FORM:

17 (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage

18 (B) COMPUTER: Dell PC

19 (C) OPERATING SYSTEM: MS DOS

20 (D) SOFTWARE: Microsoft Word version 97

21 (vi) CURRENT APPLICATION DATA:

C--> 22 (A) APPLICATION NUMBER: US/09/145,916B

C--> 23 (B) FILING DATE: 02-Sep-1998

24 (C) CLASSIFICATION: Unknown

25 (viii) ATTORNEY/AGENT INFORMATION:

26 (A) NAME: David Prashker, Esq.

27 (B) REGISTRATION NUMBER: 29,693

28 (C) REFERENCE/DOCKET NUMBER: BIS-039

29 (ix) TELECOMMUNICATION INFORMATION:

30 (A) TELEPHONE: (978) 525-3794

31 (2) INFORMATION FOR SEQ ID NO: 1:

32 (i) SEQUENCE CHARACTERISTICS:

33 (A) LENGTH: 762 base pairs

34 (B) TYPE: nucleic acid

35 (C) STRANDEDNESS: single

36 (D) TOPOLOGY: linear

37 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

39 ATGAGACGTG CGGCGCTCTG GCTTTGGCTC TGCGCGCTGG CGCTGCGCCT GCAGCCTGCC 60
 40 CTCCCGCAA TTGTACCGC AAATGTGCCT CCTGAAGACC AAGATGGCTC TGGGGACGAC 120
 41 TCAGACAACT TCTCTGGCTC AGGCACAGGT GCTTTGCCAG ATATGACTTT GTCACGGCAG 180
 42 ACACCTTCCA CTTGGAAGGA TGTGTGGCTC CTGACAGCTA CACCCACAGC TCCAGAACCC 240
 43 ACCAGCAGGG ATACCGAGGC CACCCTCACC TCTATCCTGC CGGCTGGAGA GAAGCCTGAG 300
 44 GAGGGAGAGC CCGTGGCCCA CGTGAAGCA GAGCCTGACT TCACTGCTCG GGACAAGGAG 360
 45 AAGGAGGCCA CCACCAGGCC TAGGGAGACC ACACAGCTCC CAGTCAACCA ACAGGCCTCA 420
 46 ACAGCAGCCA GAGCCACCAC GGCCCAGGCA TCTGTCACGT CTCATCCCCA CGGGGATGTG 480
 47 CAACCTGGCC TCCACGAGAC CTTGGCTCCC ACAGCACCCG GCCAACCTGA CCATCAGCCT 540

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48 CCAAGTGTGG AGGATGGAGG CACTTCTGTC ATCAAAGAGG TTGTGGAGGA TGAAACTACC 600
 49 AATCAGCTTC CTGCAGGAGA GGGCTCTGGA GAACAAGACT TCACCTTTGA AACATCTGGG 660
 50 GAGAACACAG CTGTGGCTGG CGTCGAGCCT GACCTTCGGA ATCAGTCCCC AGTGGATGAA 720
 51 GGAGCCACAG GTGCTTCTCA GGGCCTTTTG GACAGGAAGG AA 762

53 (2) INFORMATION FOR SEQ ID NO: 2:

54 (i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 1020 base pairs

56 (B) TYPE: nucleic acid

57 (C) STRANDEDNESS: single

58 (D) TOPOLOGY: linear

59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

61 GGCAGGAGGG AGGGAGCCAG AGGAAAAGAA GAGGAGGAGA AGGAGGAGGA CCCGGGGAGG 60
 62 GAGGCGCGGC GCGGGAGGAG GAGGGGCGCA GCCGCGGAGC CAGTGGCCCC GCTTGGACGC 120
 63 GCTGCTCTCC AGATACCCCC GGAGCTCCAG CCGCGCGGAT CGCGCGCTCC CGCCGCTCTG 180
 64 CCCCTAAACT TCTGCCGTAG CTCCCTTTCA AGCCAGCGAA TTTATTCCTT AAAACCAGAA 240
 65 ACTGAACCTC GGCACGGGAA AGGAGTCCGC GGAGGAGCAA AACCACAGCA GAGCAAGAAG 300
 66 AGCTTCAGAG AGCAGCCTTC CCGGAGCACC AACTCCGTGT CGGGAGTGCA GAAACCAACA 360
 67 AGTGAGAGGG CGCCGCGTTC CCGGGGCGCA GCTGCGGGCG GCGGGAGCAG GCGCAGGAGG 420
 68 AGGAAGCGAG CGCCCCGAG CCCCGAGCCC GAGTCCCCGA GCCTGAGCCG CAATCGCTGC 480
 69 GGTACTCTGC TCCGGATTCTG TGTGCGCGGG CTCGCCGAGC GCTGGGCAGG AGGCTTCGTT 540
 70 TTGCCCTGGT TGCAAGCAGC GGCTGGGAGC AGCCGGTCCC TGGGGAATAT GCGGCGCGCG 600
 71 TGGATCCTGC TCACCTTGGG CTTGGTGGCC TGCGTGTCGG CGGAGTCGAG AGCAGAGCTG 660
 72 ACATCTGATA AAGACATGTA CCTTGACAAC AGCTCCATTG AAGAAGCTTC AGGAGTGTAT 720
 73 CCTATTGATG ACGATGACTA CGCTTCTGCG TCTGGCTCGG GAGCTGATGA GGATGTAGAG 780
 74 AGTCCAGAGC TGACAACAAC TCGACCACTT CCAAAGATAC TGTTGACTAG TGCTGCTCCA 840
 75 AAAGTGGAAA CCACGACGCT GAATATACAG AACAAAGATAC CTGCTCAGAC AAAGTCACCT 900
 76 GAAGAAACTG ATAAAGAGAA AGTTCACCTC TCTGACTCAG AAAGGAAAAT GGACCCAGCC 960
 77 GAAGAGGATA CAAATGTGTA TACTGAGAAA CACTCAGACA GTCTGTTTAA ACGGACAGAA 1020

79 (2) INFORMATION FOR SEQ ID NO: 3:

80 (i) SEQUENCE CHARACTERISTICS:

81 (A) LENGTH: 340 amino acids

82 (B) TYPE: amino acid

83 (C) STRANDEDNESS: single

84 (D) TOPOLOGY: linear

85 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

87 Gly Arg Arg Glu Gly Ala Arg Gly Lys Glu Glu Glu Glu Lys Glu Glu
 88 1 5 10 15
 89 Asp Pro Gly Arg Glu Ala Arg Arg Gly Arg Arg Arg Gly Ala Ala Ala
 90 20 25 30
 91 Glu Pro Val Ala Pro Leu Gly Arg Ala Ala Leu Gln Ile Pro Pro Glu
 92 35 40 45
 93 Leu Gln Pro Arg Gly Ser Arg Ala Pro Ala Ala Leu Pro Leu Asn Phe
 94 50 55 60
 95 Cys Arg Ser Ser Leu Ser Ser Gln Arg Ile Tyr Ser Leu Lys Pro Glu
 96 65 70 75 80
 97 Thr Glu Pro Arg His Gly Lys Gly Val Arg Gly Gly Ala Lys Pro Gln
 98 85 90 95
 99 Gln Ser Lys Lys Ser Phe Arg Glu Gln Pro Ser Arg Ser Thr Asn Ser
 100 100 105 110

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```

101 Val Ser Gly Val Gln Lys Pro Thr Ser Glu Arg Ala Pro Arg Ser Arg
102      115      120      125
103 Gly Ala Ala Ala Gly Gly Gly Ser Arg Arg Arg Arg Arg Lys Arg Ala
104      130      135      140
105 Pro Pro Ser Pro Glu Pro Glu Ser Pro Ser Leu Ser Arg Asn Arg Cys
106 145      150      155      160
107 Gly Thr Leu Leu Arg Ile Arg Val Arg Gly Leu Ala Glu Arg Trp Ala
108      165      170      175
109 Gly Gly Phe Val Leu Pro Trp Leu Gln Ala Ala Ala Gly Ser Ser Arg
110      180      185      190
111 Ser Leu Gly Asn Met Arg Arg Ala Trp Ile Leu Leu Thr Leu Gly Leu
112      195      200      205
113 Val Ala Cys Val Ser Ala Glu Ser Arg Ala Glu Leu Thr Ser Asp Lys
114      210      215      220
115 Asp Met Tyr Leu Asp Asn Ser Ser Ile Glu Glu Ala Ser Gly Val Tyr
116 225      230      235      240
117 Pro Ile Asp Asp Asp Asp Tyr Ala Ser Ala Ser Gly Ser Gly Ala Asp
118      245      250      255
119 Glu Asp Val Glu Ser Pro Glu Leu Thr Thr Thr Arg Pro Leu Pro Lys
120      260      265      270
121 Ile Leu Leu Thr Ser Ala Ala Pro Lys Val Glu Thr Thr Thr Leu Asn
122      275      280      285
123 Ile Gln Asn Lys Ile Pro Ala Gln Thr Lys Ser Pro Glu Glu Thr Asp
124      290      295      300
125 Lys Glu Lys Val His Leu Ser Asp Ser Glu Arg Lys Met Asp Pro Ala
126 305      310      315      320
127 Glu Glu Asp Thr Asn Val Tyr Thr Glu Lys His Ser Asp Ser Leu Phe
128      325      330      335
129 Lys Arg Thr Glu
130      340

```

132 (2) INFORMATION FOR SEQ ID NO: 4:

133 (i) SEQUENCE CHARACTERISTICS:

134 (A) LENGTH: 1079 base pairs

135 (B) TYPE: nucleic acid

136 (C) STRANDEDNESS: single

137 (D) TOPOLOGY: linear

138 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```

140 GCCCCGCGC GCTGCTGAGC CGTCCTTGCG GCACGSSGAT GCCCCGCGGAG CTGCGGCGCC 60
141 TCGCGGTGCT GCTGCTGCTG CTCAGCGCCC GCGCAGCGCT GGCTCAGCCG TGGCGCAATG 120
142 AGAACTACGA GAGGCCGGTG GACCTGGAGG GCTCTGGGGA TGATGATCCC TTTGGGGACG 180
143 ATGAACTGGA TGACATCTAC TCGGGCTCCG GCTCAGGCTA TTTTGAGCAG GAGTCAGGGT 240
144 TGGAGACAGC GGTACGCCTC ACCACGGACA CGTCCGTCCC ACTGCCACC ACGGTGGCCG 300
145 TGCTGCCTGT CACCTTGGTG CAGCCCATGG CAACACCCTT TGAGCTGTTC CCCACAGAGG 360
146 ACACGTCCCC TGAGCAAACA ACCAGCGTCT TGTATATCCC CAAGATAACA GAAGCACCAG 420
147 TGATCCCCAG CTGGAACAACA ACCACGCCA GTACCACTGC CAGTGACTCC CCCAGTACCA 480
148 CCTCCACCAC CACCACCACG GCTGCTACCA CCACCACAAC CACCACCACC ATCAGACCA 540
149 CTGTGGCCAC CTCCAAGCCC ACCACTACCC AGAGGTTTCT GCCCCCTTT GTCACCAAGG 600
150 CAGCCACCAC CCGGGCCACC ACCCTGGAGA CGCCACCAC CTCCATCCCT GAAACCAGTG 660
151 TCCTGACAGA GGTGACCACA TCACGGCTTG TCCCCTCCAG CACAGCCAAG CCGAGGTCCC 720

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152 TGCCAAACC AAGCACTTCC AGGACTGCAG AACCCACGGA AAAAAGCACT GCCTTGCCCTT 780
153 CCAGCCCCAC CACGCTGCCA CCCACAGAAG CCCCCCAGGT GGAGCCAGGG GAGTTGACGA 840
154 CAGTCCTCGA CAGTGACCTG GAAGTCCCAA CCAGTAGTGG CCCCAGCGGG GACTTCGAGA 900
155 TCCAGGAGGA GGAGGAGACA ACTCGTCCTG AGCTGGGCAA TGAGGTGGTG GCAGTGGTGA 960
156 CACCACCAGC AGCACCAGGG CTGGGCAAGA ATGCAGAGCC GGGGCTCATC GACAACACAA 1020
157 TAGAGTCGGG CAGCTCGGCT GCTCAGCTCC CCCAGAAAAA CATCCTGGAG AGGAAGGAA 1079
159 (2) INFORMATION FOR SEQ ID NO: 5:
160     (i) SEQUENCE CHARACTERISTICS:
161         (A) LENGTH: 447 base pairs
162         (B) TYPE: nucleic acid
163         (C) STRANDEDNESS: single
164         (D) TOPOLOGY: linear
165     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
167 ATGGCGCCTG TCTGCCTGTT TGCGCCGCTG CTGCTGTTGC TCCTCGGAGG TTTCCCCGTC 60
168 GCCCCAGGCG AGTCGATTCG AGAGACTGAG GTCATAGACC CCCAGGACCT CCTGGAAGGC 120
169 AGATACTTCT CTGGAGCCCT CCCGGACGAT GAAGACGCTG GGGGCCCTGA GCAGGACTCT 180
170 GACTTTGAGC TGTCGGGTTC CGGAGATCTA GATGACACGG AGGAGCCCAG GACCTTCCCT 240
171 GAGGTGATTT CACCCTTGGT GCCACTAGAT AACCACATCC CCGAGAATGC CCAGCCTGGC 300
172 ATCCGTGTCC CCTCAGAGCC CAAGGAAGTG GAAGAGAATG AGGTCATTCC CAAAAGGGTC 360
173 CCCTCCGACG TGGGGGATGA CGATGTGTCC AACAAAGTGT CCATGTCCAG CACTTCCCAG 420
174 GGCAGCAACA TTTTGTAAAG AACTGAG                                     447
176 (2) INFORMATION FOR SEQ ID NO: 6:
177     (i) SEQUENCE CHARACTERISTICS:
178         (A) LENGTH: 1590 base pairs
179         (B) TYPE: nucleic acid
180         (C) STRANDEDNESS: single
181         (D) TOPOLOGY: linear
182     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
184 ATGGAGCTCC GGGCCCGAGG CTGGTGCTG CTGTGCGCGG CCGCCGCGCT AGTCGCCTGC 60
185 GCCCGCGGGG ACCCCGCCAG CAAGAGCCGG AGCTGCAGCG AAGTCCGCCA GATCTACGGG 120
186 GCTAAGGGCT TTAGCCTGAG CGACGTGCCC CAGGCAGAGA TCTCGGGAGA GCACCTGCGG 180
187 ATCTGCCCCC AGGGCTACAC CTGCTGCACC AGTGAGATGG AGGAGAACCT GGCCAACCAC 240
188 AGCCGGATGG AGCTGGAGAC CGCACTCCAC GACAGCAGCC GTGCCCTGCA GGCTACACTG 300
189 GCCACCCAGC TGCATGGCAT CGATGACCAC TTCCAGCGCC TGCTGAATGA CTCGGAGCGT 360
190 ACACTGCAGG ATGCTTTTCC CGGGGCCTTT GGGGACCTGT ACACGCAGAA CACTCGGGCC 420
191 TTCCGGGACC TGTATGCTGA GCTGCGTCTC TACTACCGAG GGGCCAACCT ACACCTTGAG 480
192 GAGACACTGG CCGAGTTCTG GGCACGGCTG CTGGAGCGTC TCTTCAAGCA GCTGCACCCC 540
193 CAGCTTCTGC TGCCCGATGA CTATCTGGAC TGCCTGGGCA AGCAGGCAGA GGCACTGCGG 600
194 CCGTTTGGGG ATGCCCTCG AGAACTGCGC CTGAGGGCCA CCCGTGCTTT TGTGGCGGCA 660
195 CGATCCTTTG TGCAGGGCCT GGGTGTGGCC AGTGACGTAG TCCGAAAGGT GGCCAGGTT 720
196 CACTCTGGCCC CAGAATGTTT TCGGGCTGTC ATGAAGTTGG TCTACTGTGC CCATTGCCGG 780
197 GGAGTCCCTG GTGCCCCGCC CTGTCCCAG TATTGCCGAA ATGTGCTCAA AGGCTGCCTT 840
198 GCCAACCAGG CCGACCTGGA TGCCGAGTGG AGGAACCTCC TGGACTCCAT GGTGCTCATC 900
199 ACTGACAAGT TCTGGGGCCC GTCGGGTGCG GAGAATGTCA TTGGCAGTGT GCATATGTGG 960
200 CTGGCGGAGG CCATCAACGC CCTCCAGGAC AACAAGGACA CACTCACAGC TAAGGTCATC 1020
201 CAGGGCTGCG GAAACCCCAA GGTCAATCCC CATGGCTCTG GGCCTGAGGA GAAGCGTCGC 1080
202 CGTGGCAAAC TGGCACTGCA GGAGAAGTCC TCCACAGGTA CTCTGGAAAA GCTGGTCTCT 1140
203 GAGGCCAAGG CCCAGCTCCG AGACATTAG GACTACTGGA TCAGCCTCCC AGGGACACTG 1200
204 TGAGTGAGA AGATGGCCAT GAGTCCTGCC AGCGATGACC GCTGCTGGAA TGGGATTTCC 1260

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205 AAGGGCCGGT ACCTACCTGA GGTGATGGGT GATGGGCTGG CCAACCAGAT CAACAACCCT 1320
206 GAAGTGGAGG TGGACATCAC CAAGCCGGAT ATGACCATCC GGCAGCAGAT CATGCAGCTC 1380
207 AAGATCATGA CCAACCGTTT ACGTGGCGCC TACGGTGGCA ATGATGTGGA CTTCCAGGAT 1440
208 GCCAGTGATG ACGGCAGTGG CTCCGGCAGC GGTGGCGGAT GCCCAGATGA CGCCTGTGGC 1500
209 CGGAGGGTCA GCAAGAAGAG CTCCAGCTCC CGGACCCCTT TGACCCATGC CCTCCCCGGC 1560
210 TTGTCAGAAC AGGAGGGACA GAAGACCTCG                                     1590
212 (2) INFORMATION FOR SEQ ID NO: 7:
213     (i) SEQUENCE CHARACTERISTICS:
214         (A) LENGTH: 531 amino acids
215         (B) TYPE: amino acid
216         (C) STRANDEDNESS: single
217         (D) TOPOLOGY: linear
218     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
220 Met Glu Leu Arg Ala Arg Gly Trp Trp Leu Leu Cys Ala Ala Ala Ala
221 1      5      10      15
222 Leu Val Ala Cys Ala Arg Gly Asp Pro Ala Ser Lys Ser Arg Ser Cys
223      20      25      30
224 Ser Glu Val Arg Gln Ile Tyr Gly Ala Lys Gly Phe Ser Leu Ser Asp
225      35      40      45
226 Val Pro Gln Ala Glu Ile Ser Gly Glu His Leu Arg Ile Cys Pro Gln
227      50      55      60
228 Gly Tyr Thr Cys Cys Thr Ser Glu Met Glu Glu Asn Leu Ala Asn His
229 65      70      75      80
230 Ser Arg Met Glu Leu Glu Thr Ala Leu His Asp Ser Ser Arg Ala Leu
231      85      90      95
232 Gln Ala Thr Leu Ala Thr Gln Leu His Gly Ile Asp Asp His Phe Gln
233     100     105     110
234 Arg Leu Leu Asn Asp Ser Glu Arg Thr Leu Gln Asp Ala Phe Pro Gly
235     115     120     125
236 Ala Phe Gly Asp Leu Tyr Thr Gln Asn Thr Arg Ala Phe Arg Asp Leu
237     130     135     140
238 Tyr Ala Glu Leu Arg Leu Tyr Tyr Arg Gly Ala Asn Leu His Leu Glu
239 145     150     155     160
240 Glu Thr Leu Ala Glu Phe Trp Ala Arg Leu Leu Glu Arg Leu Phe Lys
241     165     170     175
242 Gln Leu His Pro Gln Leu Leu Leu Pro Asp Asp Tyr Leu Asp Cys Leu
243     180     185     190
244 Gly Lys Gln Ala Glu Ala Leu Arg Pro Phe Gly Asp Ala Pro Arg Glu
245     195     200     205
246 Leu Arg Leu Arg Ala Thr Arg Ala Phe Val Ala Ala Arg Ser Phe Val
247     210     215     220
248 Gln Gly Leu Gly Val Ala Ser Asp Val Val Arg Lys Val Ala Gln Val
249 225     230     235     240
250 Pro Leu Ala Pro Glu Cys Ser Arg Ala Val Met Lys Leu Val Tyr Cys
251     245     250     255
252 Ala His Cys Arg Gly Val Pro Gly Ala Arg Pro Cys Pro Asp Tyr Cys
253     260     265     270
254 Arg Asn Val Leu Lys Gly Cys Leu Ala Asn Gln Ala Asp Leu Asp Ala
255     275     280     285

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VERIFICATION SUMMARY

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L:22 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:23 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]